

Sequence listing

<110> Pieris Proteolab AG

<120> Soluble truncated polypeptides of the Nogo-A protein, methods for the production of such polypeptides and methods for identifying compounds having detectable affinity to a Nogo-A protein

<160> 18

<210> 1

<211> 1163

<212> PRT

<213> rat

<220>

<223> rat Nogo-A protein

<400> 1

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			20						25					30

Glu	Pro	Glu	Asp	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Glu
			35						40					45

Glu	Asp	Asp	Glu	Asp	Leu	Glu	Glu	Leu	Glu	Val	Leu	Glu	Arg	Lys
			50						55					60

Pro	Ala	Ala	Gly	Leu	Ser	Ala	Ala	Ala	Val	Pro	Pro	Ala	Ala	Ala
			65						70					75

Ala	Pro	Leu	Leu	Asp	Phe	Ser	Ser	Asp	Ser	Val	Pro	Pro	Ala	Pro
			80						85					90

Arg	Gly	Pro	Leu	Pro	Ala	Ala	Pro	Pro	Ala	Ala	Pro	Glu	Arg	Gln
			95						100					105

Pro	Ser	Trp	Glu	Arg	Ser	Pro	Ala	Ala	Pro	Ala	Pro	Ser	Leu	Pro
			110						115					120

Pro	Ala	Ala	Ala	Val	Leu	Pro	Ser	Lys	Leu	Pro	Glu	Asp	Asp	Glu
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Pro	Pro	Ala	Arg	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Gly	Ala	Ser	Pro
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Leu	Ala	Glu	Pro	Ala	Ala	Pro	Pro	Ser	Thr	Pro	Ala	Ala	Pro	Lys
			155						160					165

Arg	Arg	Gly	Ser	Gly	Ser	Val	Asp	Glu	Thr	Leu	Phe	Ala	Leu	Pro
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Ala	Ala	Ser	Glu	Pro	Val	Ile	Pro	Ser	Ser	Ala	Glu	Lys	Ile	Met
			185						190					195

Asp	Leu	Met	Glu	Gln	Pro	Gly	Asn	Thr	Val	Ser	Ser	Gly	Gln	Glu
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				200						205				210	
Asp	Phe	Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Leu	Pro	Ser	
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Leu	Ser	Pro	Leu	Ser	Thr	Val	Ser	Phe	Lys	Glu	His	Gly	Tyr	Leu	
				230					235					240	
Gly	Asn	Leu	Ser	Ala	Val	Ser	Ser	Ser	Glu	Gly	Thr	Ile	Glu	Glu	
				245					250					255	
Thr	Leu	Asn	Glu	Ala	Ser	Lys	Glu	Leu	Pro	Glu	Arg	Ala	Thr	Asn	
				260					265					270	
Pro	Phe	Val	Asn	Arg	Asp	Leu	Ala	Glu	Phe	Ser	Glu	Leu	Glu	Tyr	
				275					280					285	
Ser	Glu	Met	Gly	Ser	Ser	Phe	Lys	Gly	Ser	Pro	Lys	Gly	Glu	Ser	
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Ala	Ile	Leu	Val	Glu	Asn	Thr	Lys	Glu	Glu	Val	Ile	Val	Arg	Ser	
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Lys	Asp	Lys	Glu	Asp	Leu	Val	Cys	Ser	Ala	Ala	Leu	His	Ser	Pro	
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Gln	Glu	Ser	Pro	Val	Gly	Lys	Glu	Asp	Arg	Val	Val	Ser	Pro	Glu	
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Lys	Thr	Met	Asp	Ile	Phe	Asn	Glu	Met	Gln	Met	Ser	Val	Val	Ala	
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Pro	Val	Arg	Glu	Glu	Tyr	Ala	Asp	Phe	Lys	Pro	Phe	Glu	Gln	Ala	
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Trp	Glu	Val	Lys	Asp	Thr	Tyr	Glu	Gly	Ser	Arg	Asp	Val	Leu	Ala	
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Ala	Arg	Ala	Asn	Val	Glu	Ser	Lys	Val	Asp	Arg	Lys	Cys	Leu	Glu	
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Asp	Ser	Leu	Glu	Gln	Lys	Ser	Leu	Gly	Lys	Asp	Ser	Glu	Gly	Arg	
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Asn	Glu	Asp	Ala	Ser	Phe	Pro	Ser	Thr	Pro	Glu	Pro	Val	Lys	Asp	
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Ser	Ser	Arg	Ala	Tyr	Ile	Thr	Cys	Ala	Ser	Phe	Thr	Ser	Ala	Thr	
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Glu	Ser	Thr	Thr	Ala	Asn	Thr	Phe	Pro	Leu	Leu	Glu	Asp	His	Thr	
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Ser	Glu	Asn	Lys	Thr	Asp	Glu	Lys	Lys	Ile	Glu	Glu	Arg	Lys	Ala	
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Gln	Ile	Ile	Thr	Glu	Lys	Thr	Ser	Pro	Lys	Thr	Ser	Asn	Pro	Phe	
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Leu	Val	Ala	Val	Gln	Asp	Ser	Glu	Ala	Asp	Tyr	Val	Thr	Thr	Asp	
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Thr	Leu	Ser	Lys	Val	Thr	Glu	Ala	Ala	Val	Ser	Asn	Met	Pro	Glu	

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Gly	Leu	Thr	Pro	Asp	Leu	Val	Gln	Glu	Ala	Cys	Glu	Ser	Glu	Leu
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Asn	Glu	Ala	Thr	Gly	Thr	Lys	Ile	Ala	Tyr	Glu	Thr	Lys	Val	Asp
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Leu	Val	Gln	Thr	Ser	Glu	Ala	Ile	Gln	Glu	Ser	Leu	Tyr	Pro	Thr
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Ala	Gln	Leu	Cys	Pro	Ser	Phe	Glu	Glu	Ala	Glu	Ala	Thr	Pro	Ser
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Pro	Val	Leu	Pro	Asp	Ile	Val	Met	Glu	Ala	Pro	Leu	Asn	Ser	Leu
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Leu	Pro	Ser	Ala	Gly	Ala	Ser	Val	Val	Gln	Pro	Ser	Val	Ser	Pro
				605					610					615
Leu	Glu	Ala	Pro	Pro	Pro	Val	Ser	Tyr	Asp	Ser	Ile	Lys	Leu	Glu
				620					625					630
Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu	Ala	Met	Asn	Val	Ala	Leu
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Lys	Ala	Leu	Gly	Thr	Lys	Glu	Gly	Ile	Lys	Glu	Pro	Glu	Ser	Phe
				650					655					660
Asn	Ala	Ala	Val	Gln	Glu	Thr	Glu	Ala	Pro	Tyr	Ile	Ser	Ile	Ala
				665					670					675
Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser	Thr	Glu	Pro	Ser	Pro
				680					685					690
Asp	Phe	Ser	Asn	Tyr	Ser	Glu	Ile	Ala	Lys	Phe	Glu	Lys	Ser	Val
				695					700					705
Pro	Glu	His	Ala	Glu	Leu	Val	Glu	Asp	Ser	Ser	Pro	Glu	Ser	Glu
				710					715					720
Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser	Ile	Pro	Glu	Val	Pro	Gln
				725					730					735
Thr	Gln	Glu	Glu	Ala	Val	Met	Leu	Met	Lys	Glu	Ser	Leu	Thr	Glu
				740					745					750
Val	Ser	Glu	Thr	Val	Ala	Gln	His	Lys	Glu	Glu	Arg	Leu	Ser	Ala
				755					760					765
Ser	Pro	Gln	Glu	Leu	Gly	Lys	Pro	Tyr	Leu	Glu	Ser	Phe	Gln	Pro
				770					775					780
Asn	Leu	His	Ser	Thr	Lys	Asp	Ala	Ala	Ser	Asn	Asp	Ile	Pro	Thr
				785					790					795
Leu	Thr	Lys	Lys	Glu	Lys	Ile	Ser	Leu	Gln	Met	Glu	Glu	Phe	Asn
				800					805					810
Thr	Ala	Ile	Tyr	Ser	Asn	Asp	Asp	Leu	Leu	Ser	Ser	Lys	Glu	Asp
				815					820					825
Lys	Ile	Lys	Glu	Ser	Glu	Thr	Phe	Ser	Asp	Ser	Ser	Pro	Ile	Glu

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Ile	Ile	Asp	Glu	Phe	Pro	Thr	Phe	Val	Ser	Ala	Lys	Asp	Asp	Ser
				845					850					855
Pro	Lys	Leu	Ala	Lys	Glu	Tyr	Thr	Asp	Leu	Glu	Val	Ser	Asp	Lys
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Ser	Glu	Ile	Ala	Asn	Ile	Gln	Ser	Gly	Ala	Asp	Ser	Leu	Pro	Cys
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Leu	Glu	Leu	Pro	Cys	Asp	Leu	Ser	Phe	Lys	Asn	Ile	Tyr	Pro	Lys
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Val	Ser	Lys	Ala	Ser	Ile	Ser	Pro	Ser	Asn	Val	Ser	Ala	Leu	Glu
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Arg	Ser	Leu	Ser	Ala	Val	Leu	Ser	Ala	Glu	Leu	Ser	Lys	Thr	Ser
				965					970					975
Val	Val	Asp	Leu	Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Lys	Thr	Gly	Val
				980					985					990
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				995					1000					1005
Ser	Ile	Val	Ser	Val	Thr	Ala	Tyr	Ile	Ala	Leu	Ala	Leu	Leu	Ser
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Val	Thr	Ile	Ser	Phe	Arg	Ile	Tyr	Lys	Gly	Val	Ile	Gln	Ala	Ile
				1030					1030					1035
Gln	Lys	Ser	Asp	Glu	Gly	His	Pro	Phe	Arg	Ala	Tyr	Leu	Glu	Ser
				1040					1045					1050
Glu	Val	Ala	Ile	Ser	Glu	Glu	Leu	Val	Gln	Lys	Tyr	Ser	Asn	Ser
				1055					1060					1065
Ala	Leu	Gly	His	Val	Asn	Ser	Thr	Ile	Lys	Glu	Leu	Arg	Arg	Leu
				1070					1075					1080
Phe	Leu	Val	Asp	Asp	Leu	Val	Asp	Ser	Leu	Lys	Phe	Ala	Val	Leu
				1085					1090					1095
Met	Trp	Val	Phe	Thr	Tyr	Val	Gly	Ala	Leu	Phe	Asn	Gly	Leu	Thr
				1100					1105					1110
Leu	Leu	Ile	Leu	Ala	Leu	Ile	Ser	Leu	Phe	Ser	Ile	Pro	Val	Ile
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Tyr	Glu	Arg	His	Gln	Val	Gln	Ile	Asp	His	Tyr	Leu	Gly	Leu	Ala
				1130					1135					1140
Asn	Lys	Ser	Val	Lys	Asp	Ala	Met	Ala	Lys	Ile	Gln	Ala	Lys	Ile

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1150

1155

Pro Gly Leu Lys Arg Lys Ala Asp
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<210> 2

<211> 1192

<212> PRT

<213> human

<220>

<223> human Nogo-A protein

<400> 2

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Pro	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Glu	35	40	45	
Asp	Glu	Asp	Leu	Glu	Glu	Leu	Glu	Val	Leu	Glu	Arg	Lys	Pro	Ala	50	55	60	
Ala	Gly	Leu	Ser	Ala	Ala	Pro	Val	Pro	Thr	Ala	Pro	Ala	Ala	Gly	65	70	75	
Ala	Pro	Leu	Met	Asp	Phe	Gly	Asn	Glu	Phe	Val	Pro	Pro	Ala	Pro	80	85	90	
Arg	Gly	Pro	Leu	Pro	Ala	Ala	Pro	Pro	Val	Ala	Pro	Glu	Arg	Gln	95	100	105	
Pro	Ser	Trp	Asp	Pro	Ser	Pro	Val	Ser	Ser	Thr	Val	Pro	Ala	Pro	110	115	120	
Ser	Pro	Leu	Ser	Ala	Ala	Ala	Val	Ser	Pro	Ser	Lys	Leu	Pro	Glu	125	130	135	
Asp	Asp	Glu	Pro	Pro	Ala	Arg	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Ser	140	145	150	
Val	Ser	Pro	Gln	Ala	Glu	Pro	Val	Trp	Thr	Pro	Pro	Ala	Pro	Ala	155	160	165	
Pro	Ala	Ala	Pro	Pro	Ser	Thr	Pro	Ala	Ala	Pro	Lys	Arg	Arg	Gly	170	185	180	
Ser	Ser	Gly	Ser	Val	Asp	Glu	Thr	Leu	Phe	Ala	Leu	Pro	Ala	Ala	185	190	195	
Ser	Glu	Pro	Val	Ile	Arg	Ser	Ser	Ala	Glu	Asn	Met	Glu	Leu	Lys	200	205	210	
Glu	Gln	Pro	Gly	Asn	Thr	Ile	Ser	Ala	Gly	Gln	Glu	Asp	Phe	Pro	215	220	225	
Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Leu	Pro	Ser	Leu	Ser	Pro				

				230					235					240
Leu	Ser	Ala	Ala	Ser 245	Phe	Lys	Glu	His	Glu 250	Tyr	Leu	Glu	Asn	Leu 255
Ser	Thr	Val	Leu	Pro 260	Thr	Glu	Gly	Thr	Leu 265	Gln	Glu	Asn	Val	Ser 270
Glu	Ala	Ser	Lys	Glu 275	Val	Ser	Glu	Lys	Ala 280	Lys	Thr	Leu	Leu	Ile 285
Asp	Arg	Asp	Leu	Thr 290	Glu	Phe	Ser	Glu	Leu 295	Glu	Tyr	Ser	Glu	Met 300
Gly	Ser	Ser	Phe	Ser 305	Val	Ser	Pro	Lys	Ala 310	Glu	Ser	Ala	Val	Ile 315
Val	Ala	Asn	Pro	Arg 320	Glu	Glu	Ile	Ile	Val 325	Lys	Asn	Lys	Asp	Glu 330
Glu	Glu	Lys	Leu	Val 335	Ser	Asn	Ans	Ile	Leu 340	His	Asn	Gln	Gln	Glu 345
Leu	Pro	Thr	Ala	Leu 350	Thr	Lys	Leu	Val	Lys 355	Glu	Asp	Glu	Val	Val 360
Ser	Ser	Glu	Lys	Ala 365	Lys	Asp	Ser	Phe	Asn 370	Glu	Lys	Arg	Val	Ala 385
Val	Glu	Ala	Pro	Met 380	Arg	Glu	Glu	Tyr	Ala 385	Asp	Phe	Lys	Pro	Phe 390
Glu	Arg	Val	Trp	Glu 395	Val	Lys	Asp	Ser	Lys 400	Glu	Asp	Ser	Asp	Met 405
Leu	Ala	Ala	Gly	Gly 410	Lys	Ile	Glu	Ser	Asn 415	Leu	Glu	Ser	Lys	Val 420
Asp	Lys	Lys	Cys	Phe 425	Ala	Asp	Ser	Leu	Glu 430	Gln	Thr	Asn	His	Glu 435
Lys	Asn	Ser	Glu	Ser 440	Ser	Asn	Asp	Asp	Thr 445	Ser	Phe	Pro	Ser	Thr 450
Pro	Glu	Gly	Ile	Lys 455	Asp	Arg	Pro	Gly	Ala 460	Tyr	Ile	Thr	Cys	Ala 465
Pro	Phe	Asn	Pro	Ala 470	Ala	Thr	Glu	Ser	Ile 475	Ala	Thr	Asn	Ile	Phe 480
Pro	Leu	Leu	Gly	Asp 485	Pro	Thr	Ser	Glu	Asn 490	Lys	Thr	Asp	Glu	Lys 495
Lys	Ile	Glu	Glu	Lys 500	Lys	Ala	Gln	Ile	Val 505	Thr	Glu	Lys	Asn	Thr 510
Ser	Thr	Lys	Thr	Ser 515	Asn	Pro	Phe	Leu	Val 520	Ala	Ala	Gln	Glu	Ser 525
Glu	Thr	Asp	Tyr	Val 530	Thr	Thr	Asp	Asn	Leu 535	Thr	Lys	Val	Thr	Glu 540
Glu	Val	Val	Ala	Asn	Met	Pro	Glu	Gly	Leu	Thr	Pro	Asp	Leu	Val

				545					550					555
Gln	Glu	Ala	Cys	Glu	Ser	Glu	Leu	Asn	Glu	Val	Thr	Gly	Thr	Lys
				560					565					570
Ile	Ala	Tyr	Glu	Thr	Lys	Met	Asp	Leu	Val	Gln	Thr	Ser	Glu	Val
				575					580					585
Met	Gln	Glu	Ser	Leu	Tyr	Pro	Ala	Ala	Gln	Leu	Cys	Pro	Ser	Phe
				590					595					600
Glu	Glu	Ser	Glu	Ala	Thr	Pro	Ser	Pro	Val	Leu	Pro	Asp	Ile	Val
				605					610					615
Met	Glu	Ala	Pro	Leu	Asn	Ser	Ala	Val	Pro	Ser	Ala	Gly	Ala	Ser
				620					625					630
Val	Ile	Gln	Pro	Ser	Ser	Ser	Pro	Leu	Glu	Ala	Ser	Ser	Val	Gln
				635					640					645
Tyr	Glu	Ser	Ile	Lys	His	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu
				650					655					660
Glu	Ala	Met	Ser	Val	Ser	Leu	Lys	Lys	Val	Ser	Gly	Ile	Lys	Glu
				665					670					675
Glu	Ile	Lys	Glu	Pro	Glu	Asn	Ile	Asn	Ala	Ala	Leu	Gln	Glu	Thr
				680					685					690
Glu	Ala	Pro	Tyr	Ile	Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr
				695					700					705
Lys	Leu	Ser	Ala	Glu	Pro	Ala	Pro	Glu	Phe	Ser	Asp	Tyr	Ser	Glu
				710					715					720
Met	Ala	Lys	Val	Glu	Gln	Pro	Val	Pro	Asp	His	Ser	Glu	Leu	Val
				725					730					735
Glu	Asp	Ser	Ser	Pro	Asp	Ser	Glu	Pro	Val	Asp	Leu	Phe	Ser	Asp
				740					745					750
Asp	Ser	Ile	Pro	Asp	Val	Pro	Gln	Lys	Gln	Asp	Glu	Thr	Val	Met
				755					760					765
Leu	Val	Lys	Glu	Ser	Leu	Thr	Glu	Thr	Ser	Phe	Glu	Ser	Met	Ile
				770					775					780
Glu	Tyr	Glu	Gln	Lys	Glu	Lys	Leu	Ser	Ala	Leu	Pro	Pro	Glu	Gly
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Gly	Lys	Pro	Tyr	Leu	Glu	Ser	Phe	Lys	Leu	Ser	Leu	Asp	Asn	Thr
				800					805					810
Lys	Asp	Thr	Leu	Leu	Pro	Asp	Glu	Val	Ser	Thr	Leu	Ser	Lys	Lys
				815					820					825
Glu	Lys	Ile	Pro	Ile	Gln	Met	Glu	Glu	Leu	Ser	Thr	Ala	Val	Tyr
				830					835					840
Ser	Asn	Asp	Asp	Leu	Phe	Ile	Ser	Lys	Glu	Ala	Gln	Ile	Arg	Glu
				845					850					855
Thr	Glu	Thr	Phe	Ser	Asp	Ser	Ser	Pro	Ile	Glu	Ile	Ile	Asp	Glu

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Phe Pro Thr Leu Ile Ser Ser Lys Thr	Asp Ser Phe Ser Lys Leu	
875	880	885
Ala Arg Glu Tyr Thr Asp Leu Glu Val	Ser His Lys Ser Glu Ile	
890	895	900
Ala Gln Ala Pro Asp Gly Ala Gly Ser	Leu Pro Cys Thr Glu Leu	
905	910	915
Pro His Asp Leu Ser Leu Lys Asn Ile	Gln Pro Lys Val Glu Glu	
920	925	930
Lys Ile Ser Phe Ser Asp Asp Phe Ser	Lys Asn Gly Ser Ala Thr	
935	940	945
Ser Lys Val Leu Leu Leu Pro Pro Asp	Val Ser Ala Leu Ala Thr	
950	955	960
Gln Ala Glu Ile Glu Ser Ile Val Lys	Pro Lys Val Leu Val Lys	
965	970	975
Glu Ala Glu Lys Lys Leu Pro Ser Asp	Thr Glu Lys Glu Asp Arg	
980	985	990
Ser Pro Ser Ala Ile Phe Ser Ala Glu	Leu Ser Lys Thr Ser Val	
995	1000	1005
Val Asp Leu Leu Tyr Trp Arg Asp Ile	Lys Lys Thr Gly Val Val	
1010	1015	1020
Phe Gly Ala Ser Leu Phe Leu Leu Leu	Ser Leu Thr Val Phe Ser	
1025	1030	1035
Ile Val Ser Val Thr Ala Tyr Ile Ala	Leu Ala Leu Leu Ser Val	
1040	1045	1050
Thr Ile Ser Phe Arg Ile Tyr Lys Gly	Val Ile Gln Ala Ile Gln	
1055	1060	1065
Lys Ser Asp Glu Gly His Pro Phe Arg	Ala Tyr Leu Glu Ser Glu	
1070	1075	1080
Val Ala Ile Ser Glu Glu Leu Val Gln	Lys Tyr Ser Asn Ser Ala	
1085	1090	1095
Leu Gly His Val Asn Cys Thr Ile Lys	Glu Leu Arg Arg Leu Phe	
1100	1105	1110
Leu Val Asp Asp Leu Val Asp Ser Leu	Lys Phe Ala Val Leu Met	
1115	1120	1125
Trp Val Phe Thr Tyr Val Gly Ala Leu	Phe Asn Gly Leu Thr Leu	
1130	1135	1140
Leu Ile Leu Ala Leu Ile Ser Leu Phe	Ser Val Pro Val Ile Tyr	
1145	1150	1155
Glu Arg His Gln Ala Gln Ile Asp His	Tyr Leu Gly Leu Ala Asn	
1160	1165	1170
Lys Asn Val Lys Asp Ala Met Ala Lys	Ile Gln Ala Lys Ile Pro	

1175

1180

1185

Gly Leu Lys Arg Lys Ala Glu
1190

<210> 3
<211> 33
<212> DNA
<213> artificial sequence

<220>
<223> Primer

<400> 3

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33

<210> 4
<211> 27
<212> DNA
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<400> 4

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27

<210> 5
<211> 40
<212> DNA
<213> artificial sequence

<220>
<223> Primer

<400> 5

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40

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<212> DNA
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aactatgctg ccc

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63

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<212> DNA
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<221> misc_feature
<222> (34)
<223> k: g or t

<220>
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gacattgagc tcacccagtc tccagcaatc atgkctgc 39

<210> 9
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<212> DNA
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<222> (37) ... (39)
<223> n: a, g, c or t; m: a or c

<220>
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<222> (43) ... (48)

<223> n: a, g, c or t; m: a or c

<220>
<223> Primer

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gcgcttcagc tcgagcttgg tcccagctcc gaacgtmna ggmnnmnta 50
acacattttg acagta 66

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<223> n: a, g, c or t; m: a or c

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nmnnattttg acagtaatac gttgc 74

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<223> variable domain of the heavy chain of antibody IN-1

<400> 11

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Thr	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	
				20					25					30	
Asn	Tyr	Trp	Leu	Gly	Trp	Val	Lys	Gln	Arg	Pro	Gly	His	Gly	Leu	
				35					40					45	
Glu	Trp	Ile	Gly	Asp	Ile	Tyr	Pro	Gly	Gly	Gly	Tyr	Thr	Asn	Tyr	
				50					55					60	
Asn	Glu	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Thr	Ser	
				65					70					75	
Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	
				80					85					90	
Ser	Ala	Val	Tyr	Phe	Cys	Ala	Arg	Phe	Tyr	Tyr	Gly	Ser	Ser	Tyr	
				95					100					105	
Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	
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Ser

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<223> variable domain of the light chain of the antibody II.1.8

<400> 12

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Gly Glu Thr Val Thr Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr
             20             25             30
Gly Ala Leu Asn Trp Tyr Gln Arg Lys Gln Gly Lys Ser Pro Gln
             35             40             45
Leu Leu Ile Tyr Gly Ala Thr Asn Leu Ala Asp Gly Met Ser Ser
             50             55             60
Arg Phe Ser Gly Ser Gly Ser Gly Arg Gln Tyr Ser Leu Lys Ile
             65             70             75
Ser Ser Leu His Pro Asp Asp Val Ala Thr Tyr Tyr Cys Gln Asn
             80             85             90
Ile Asn Arg Val Pro Val Thr Phe Gly Ala Gly Thr Lys Leu Glu
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Ile Lys

<210> 13

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<220>

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<222> (85)...(2238)

<223> fusion protein of truncated rat Nogo-A fragment and Strep-tag II

<220>

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<222> (85)...(2208)

<223> mature truncated Nogo-A

<220>

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<222> (2209)...(2238)

<223> Strep-tag II affinity tag

<400> 13

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45

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Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Ser Phe
                -10                                -5                                -1    1

aaa gaa cat gga tac ctt ggt aac tta tca gca gtg tca tcc tca 135
Lys Glu His Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser
                5                                10                                15

gaa gga aca att gaa gaa act tta aat gaa gct tct aaa gag ttg 180
Glu Gly Thr Ile Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu
                20                                25                                30

cca gag agg gca aca aat cca ttt gta aat aga gat tta gca gaa 225
Pro Glu Arg Ala Thr Asn Pro Phe Val Asn Arg Asp Leu Ala Glu
                35                                40                                45

ttt tca gaa tta gaa tat tca gaa atg gga tca tct ttt aaa ggc 270
Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe Lys Gly
                50                                55                                60

tcc cca aaa gga gag tca gcc ata tta gta gaa aac act aag gaa 315
Ser Pro Lys Gly Glu Ser Ala Ile Leu Val Glu Asn Thr Lys Glu
                65                                70                                75

gaa gta att gtg agg agt aaa gac aaa gag gat tta gtt tgt agt 360
Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp Leu Val Cys Ser
                80                                85                                90

gca gcc ctt cac agt cca caa gaa tca cct gtg ggt aaa gaa gac 405
Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly Lys Glu Asp
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aga gtt gtg tct cca gaa aag aca atg gac att ttt aat gaa atg 450
Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn Glu Met
                110                                115                                120

cag atg tca gta gta gca cct gtg agg gaa gag tat gca gac ttt 495
Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe
                125                                130                                135

aag cca ttt gaa caa gca tgg gaa gtg aaa gat act tat gag gga 540
Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly
                140                                145                                150

agt agg gat gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg 585
Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val
                155                                160                                165

gac aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg 630
Asp Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly
                170                                175                                180

aag gat agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc 675
Lys Asp Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr
                185                                190                                195

cca gaa cct gtg aag gac agc tcc aga gca tat att acc tgt gct 720
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tcc ttt acc tca gca acc gaa agc acc aca gca aac act ttc cct 765

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Ser	Phe	Thr 215	Ser	Ala	Thr	Glu	Ser 220	Thr	Thr	Ala	Asn	Thr 225	Phe	Pro	
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ata Ile	gaa Glu	gaa Glu 245	agg Arg	aag Lys	gcc Ala	caa Gln	att Ile 250	ata Ile	aca Thr	gag Glu	aag Lys	act Thr 255	agc Ser	ccc Pro	855
aaa Lys	acg Thr	tca Ser 260	aat Asn	cct Pro	ttc Phe	ctt Leu	gta Val 265	gca Ala	gta Val	cag Gln	gat Asp	tct Ser 270	gag Glu	gca Ala	900
gat Asp	tat Tyr	gtt Val 275	aca Thr	aca Thr	gat Asp	acc Thr	tta Leu 280	tca Ser	aag Lys	gtg Val	act Thr	gag Glu 285	gca Ala	gca Ala	945
gtg Val	tca Ser	aac Asn 290	atg Met	cct Pro	gaa Glu	ggg Gly	ctg Leu 295	acg Thr	cca Pro	gat Asp	tta Leu	gtt Val 300	cag Gln	gaa Glu	990
gca Ala	tgt Cys	gaa Glu 305	agt Ser	gaa Glu	ctg Leu	aat Asn	gaa Glu 310	gcc Ala	aca Thr	ggg Gly	aca Thr	aag Lys 315	att Ile	gct Ala	1035
tat Tyr	gaa Glu	aca Thr 320	aaa Lys	gtg Val	gac Asp	ttg Leu	gtc Val 325	caa Gln	aca Thr	tca Ser	gaa Glu	gct Ala 330	ata Ile	caa Gln	1080
gaa Glu	tca Ser	ctt Leu 335	tac Tyr	ccc Pro	aca Thr	gca Ala	cag Gln 340	ctt Leu	tgc Cys	cca Pro	tca Ser	ttt Phe 345	gag Glu	gaa Glu	1125
gct Ala	gaa Glu	gca Ala 350	act Thr	ccg Pro	tca Ser	cca Pro	gtt Val 355	ttg Leu	cct Pro	gat Asp	att Ile	gtt Val 360	atg Met	gaa Glu	1170
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cag Gln	ccc Pro	agt Ser 380	gta Val	tcc Ser	cca Pro	ctg Leu	gaa Glu 385	gca Ala	cct Pro	cct Pro	cca Pro	gtt Val 390	agt Ser	tat Tyr	1260
gac Asp	agt Ser	ata Ile 395	aag Lys	ctt Leu	gag Glu	cct Pro	gaa Glu 400	aac Asn	ccc Pro	cca Pro	cca Pro	tat Tyr 405	gaa Glu	gaa Glu	1305
gcc Ala	atg Met	aat Asn 410	gta Val	gca Ala	cta Leu	aaa Lys	gct Ala 415	ttg Leu	gga Gly	aca Thr	aag Lys	gaa Glu 420	gga Gly	ata Ile	1350
aaa Lys	gag Glu	cct Pro 425	gaa Glu	agt Ser	ttt Phe	aat Asn	gca Ala 430	gct Ala	gtt Val	cag Gln	gaa Glu	aca Thr 435	gaa Glu	gct Ala	1395
cct Pro	tat Tyr	ata Ile 440	tcc Ser	att Ile	gcg Ala	tgt Cys	gat Asp 445	tta Leu	att Ile	aaa Lys	gaa Glu	aca Thr 450	aag Lys	ctc Leu	1440

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455 460 465	
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Lys Phe Glu Lys Ser Val Pro Glu His Ala Glu Leu Val Glu Asp	
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Ser Ser Pro Glu Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser	
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Lys Glu Ser Leu Thr Glu Val Ser Glu Thr Val Ala Gln His Lys	
515 520 525	
gag gag aga ctt agt gcc tca cct cag gag cta gga aag cca tat	1710
Glu Glu Arg Leu Ser Ala Ser Pro Gln Glu Leu Gly Lys Pro Tyr	
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Leu Glu Ser Phe Gln Pro Asn Leu His Ser Thr Lys Asp Ala Ala	
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Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu Lys Ile Ser Leu	
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caa atg gaa gag ttt aat act gca att tat tca aat gat gac tta	1845
Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn Asp Asp Leu	
575 580 585	
ctt tct tct aag gaa gac aaa ata aaa gaa agt gaa aca ttt tca	1890
Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr Phe Ser	
590 595 600	
gat tca tct ccg att gag ata ata gat gaa ttt ccc acg ttt gtc	1935
Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe Val	
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Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp	
620 625 630	
cta gaa gta tcc gac aaa agt gaa att gct aat atc caa agc ggg	2025
Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly	
635 640 645	
gca gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc	2070
Ala Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe	
650 655 660	
aag aat ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc	2115
Lys Asn Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe	
665 670 675	
tcc gaa aat agg tcc agt gta tct aag gca tcc ata tcg cct tca	2160
Ser Glu Asn Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser	
680 685 690	

aat gtc tct gct ttg gaa cct cag aca gaa atg ggc agc ata gtt 2205
 Asn Val Ser Ala Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val
 695 700 705

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<220>
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 -10 -5 -1 1

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 Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu
 5 10 15

ctt ttt aaa att atg gat ttg atg gag cag cca ggt aac act gtt 225
 Leu Phe Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val
 20 25 30

tcg tct ggt caa gag gat ttc cca tct gtc ctg ctt gaa act gct 270
 Ser Ser Gly Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala
 35 40 45

gcc tct ctt cct tct cta tct cct ctc tca act gtt tct ttt aaa 315
 Ala Ser Leu Pro Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys

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Glu His Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser Glu			
65	70	75	
gga aca att gaa gaa act tta aat gaa gct tct aaa gag ttg cca 405			
Gly Thr Ile Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu Pro			
80	85	90	
gag agg gca aca aat cca ttt gta aat aga gat tta gca gaa ttt 450			
Glu Arg Ala Thr Asn Pro Phe Val Asn Arg Asp Leu Ala Glu Phe			
95	100	105	
tca gaa tta gaa tat tca gaa atg gga tca tct ttt aaa ggc tcc 495			
Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe Lys Gly Ser			
110	115	120	
cca aaa gga gag tca gcc ata tta gta gaa aac act aag gaa gaa 540			
Pro Lys Gly Glu Ser Ala Ile Leu Val Glu Asn Thr Lys Glu Glu			
125	130	135	
gta att gtg agg agt aaa gac aaa gag gat tta gtt tgt agt gca 585			
Val Ile Val Arg Ser Lys Asp Lys Glu Asp Leu Val Cys Ser Ala			
140	145	150	
gcc ctt cac agt cca caa gaa tca cct gtg ggt aaa gaa gac aga 630			
Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly Lys Glu Asp Arg			
155	160	165	
gtt gtg tct cca gaa aag aca atg gac att ttt aat gaa atg cag 675			
Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn Glu Met Gln			
170	175	180	
atg tca gta gta gca cct gtg agg gaa gag tat gca gac ttt aag 720			
Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe Lys			
185	190	195	
cca ttt gaa caa gca tgg gaa gtg aaa gat act tat gag gga agt 765			
Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly Ser			
200	205	210	
agg gat gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg gac 810			
Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp			
215	220	225	
aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg aag 855			
Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys			
230	235	240	
gat agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc cca 900			
Asp Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro			
245	250	255	
gaa cct gtg aag gac agc tcc aga gca tat att acc tgt gct tcc 945			
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ttt acc tca gca acc gaa agc acc aca gca aac act ttc cct ttg 990			
Phe Thr Ser Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu			
275	280	285	
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Tyr Val Thr Thr Asp Thr Leu Ser Lys Val Thr Glu Ala Ala Val
335                               340                               345

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Ser Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala
350                               355                               360

tgt gaa agt gaa ctg aat gaa gcc aca ggt aca aag att gct tat 1260
Cys Glu Ser Glu Leu Asn Glu Ala Thr Gly Thr Lys Ile Ala Tyr
365                               370                               375

gaa aca aaa gtg gac ttg gtc caa aca tca gaa gct ata caa gaa 1305
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380                               385                               390

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Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser Phe Glu Glu Ala
395                               400                               405

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Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala
410                               415                               420

cca tta aat tct ctc ctt cca agc gct ggt gct tct gta gtg cag 1440
Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val Val Gln
425                               430                               435

ccc agt gta tcc cca ctg gaa gca cct cct cca gtt agt tat gac 1485
Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr Asp
440                               445                               450

agt ata aag ctt gag cct gaa aac ccc cca cca tat gaa gaa gcc 1530
Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
455                               460                               465

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Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys
470                               475                               480

gag cct gaa agt ttt aat gca gct gtt cag gaa aca gaa gct cct 1620
Glu Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro
485                               490                               495

tat ata tcc att gcg tgt gat tta att aaa gaa aca aag ctc tcc 1665
Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser
500                               505                               510

act gag cca agt cca gat ttc tct aat tat tca gaa ata gca aaa 1710
Thr Glu Pro Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys
515                               520                               525

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 545 550 555

cct gaa gtc cca caa aca caa gag gag gct gtg atg ctc atg aag 1845
 Pro Glu Val Pro Gln Thr Gln Glu Glu Ala Val Met Leu Met Lys
 560 565 570

gag agt ctc act gaa gtg tct gag aca gta gcc cag cac aaa gag 1890
 Glu Ser Leu Thr Glu Val Ser Glu Thr Val Ala Gln His Lys Glu
 575 580 585

gag aga ctt agt gcc tca cct cag gag cta gga aag cca tat tta 1935
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 590 595 600

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 605 610 615

aat gac att cca aca ttg acc aaa aag gag aaa att tct ttg caa 2025
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 620 625 630

atg gaa gag ttt aat act gca att tat tca aat gat gac tta ctt 2070
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 635 640 645

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 650 655 660

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 665 670 675

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 680 685 690

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 695 700 705

gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc aag 2295
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 710 715 720

aat ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc tcc 2340
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 725 730 735

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 740 745 750

gtc tct gct ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa 2430
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 755 760 765

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<220>
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 fragment and hexahistidine tag

<220>
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<220>
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 -10 -5 -1

tgg agc cac ccg cag ttc gaa aaa ggc gcc tct ttt aaa gaa cat 135
 Trp Ser His Pro Gln Phe Glu Lys Gly Ala Ser Phe Lys Glu His
 5 10 15

gga tac ctt ggt aac tta tca gca gtg tca tcc tca gaa gga aca 180
 Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr
 20 25 30

att gaa gaa act tta aat gaa gct tct aaa gag ttg cca gag agg 225
 Ile Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg
 35 40 45

gca aca aat cca ttt gta aat aga gat tta gca gaa ttt tca gaa 270

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      65                      70                      75

gga gag tca gcc ata tta gta gaa aac act aag gaa gaa gta att 360
Gly Glu Ser Ala Ile Leu Val Glu Asn Thr Lys Glu Glu Val Ile
      80                      85                      90

gtg agg agt aaa gac aaa gag gat tta gtt tgt agt gca gcc ctt 405
Val Arg Ser Lys Asp Lys Glu Asp Leu Val Cys Ser Ala Ala Leu
      95                      100                     105

cac agt cca caa gaa tca cct gtg ggt aaa gaa gac aga gtt gtg 450
His Ser Pro Gln Glu Ser Pro Val Gly Lys Glu Asp Arg Val Val
     110                      115                     120

tct cca gaa aag aca atg gac att ttt aat gaa atg cag atg tca 495
Ser Pro Glu Lys Thr Met Asp Ile Phe Asn Glu Met Gln Met Ser
     125                      130                     135

gta gta gca cct gtg agg gaa gag tat gca gac ttt aag cca ttt 540
Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe
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gaa caa gca tgg gaa gtg aaa gat act tat gag gga agt agg gat 585
Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly Ser Arg Asp
     155                      160                     165

gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg gac aga aaa 630
Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp Arg Lys
     170                      175                     180

tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg aag gat agt 675
Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp Ser
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gaa ggc aga aat gag gat gct tct ttc ccc agt acc cca gaa cct 720
Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro
     200                      205                     210

gtg aag gac agc tcc aga gca tat att acc tgt gct tcc ttt acc 765
Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr
     215                      220                     225

tca gca acc gaa agc acc aca gca aac act ttc cct ttg tta gaa 810
Ser Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu
     230                      235                     240

gat cat act tca gaa aat aaa aca gat gaa aaa aaa ata gaa gaa 855
Asp His Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu
     245                      250                     255

agg aag gcc caa att ata aca gag aag act agc ccc aaa acg tca 900
Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser
     260                      265                     270

aat cct ttc ctt gta gca gta cag gat tct gag gca gat tat gtt 945
Asn Pro Phe Leu Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val
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aca aca gat acc tta tca aag gtg act gag gca gca gtg tca aac 990
 Thr Thr Asp Thr Leu Ser Lys Val Thr Glu Ala Ala Val Ser Asn
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atg cct gaa ggt ctg acg cca gat tta gtt cag gaa gca tgt gaa 1035
 Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu
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agt gaa ctg aat gaa gcc aca ggt aca aag att gct tat gaa aca 1080
 Ser Glu Leu Asn Glu Ala Thr Gly Thr Lys Ile Ala Tyr Glu Thr
 320 325 330

aaa gtg gac ttg gtc caa aca tca gaa gct ata caa gaa tca ctt 1125
 Lys Val Asp Leu Val Gln Thr Ser Glu Ala Ile Gln Glu Ser Leu
 335 340 345

tac ccc aca gca cag ctt tgc cca tca ttt gag gaa gct gaa gca 1170
 Tyr Pro Thr Ala Gln Leu Cys Pro Ser Phe Glu Glu Ala Glu Ala
 350 355 360

act ccg tca cca gtt ttg cct gat att gtt atg gaa gca cca tta 1215
 Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu
 365 370 375

aat tct ctc ctt cca agc gct ggt gct tct gta gtg cag ccc agt 1260
 Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val Val Gln Pro Ser
 380 385 390

gta tcc cca ctg gaa gca cct cct cca gtt agt tat gac agt ata 1305
 Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr Asp Ser Ile
 395 400 405

aag ctt gag cct gaa aac ccc cca cca tat gaa gaa gcc atg aat 1350
 Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Asn
 410 415 420

gta gca cta aaa gct ttg gga aca aag gaa gga ata aaa gag cct 1395
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gaa agt ttt aat gca gct gtt cag gaa aca gaa gct cct tat ata 1440
 Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
 440 445 450

tcc att gcg tgt gat tta att aaa gaa aca aag ctc tcc act gag 1485
 Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu
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cca agt cca gat ttc tct aat tat tca gaa ata gca aaa ttc gag 1530
 Pro Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu
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aag tcg gtg ccc gaa cac gct gag cta gtg gag gat tcc tca cct 1575
 Lys Ser Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro
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gaa tct gaa cca gtt gac tta ttt agt gat gat tcg att cct gaa 1620
 Glu Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu
 500 505 510

gtc cca caa aca caa gag gag gct gtg atg ctc atg aag gag agt 1665
 Val Pro Gln Thr Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser
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ctc act gaa gtg tct gag aca gta gcc cag cac aaa gag gag aga 1710
Leu Thr Glu Val Ser Glu Thr Val Ala Gln His Lys Glu Glu Arg
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ctt agt gcc tca cct cag gag cta gga aag cca tat tta gag tct 1755
Leu Ser Ala Ser Pro Gln Glu Leu Gly Lys Pro Tyr Leu Glu Ser
      545                      550                      555

ttt cag ccc aat tta cat agt aca aaa gat gct gca tct aat gac 1800
Phe Gln Pro Asn Leu His Ser Thr Lys Asp Ala Ala Ser Asn Asp
      560                      565                      570

att cca aca ttg acc aaa aag gag aaa att tct ttg caa atg gaa 1845
Ile Pro Thr Leu Thr Lys Lys Glu Lys Ile Ser Leu Gln Met Glu
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gag ttt aat act gca att tat tca aat gat gac tta ctt tct tct 1890
Glu Phe Asn Thr Ala Ile Tyr Ser Asn Asp Asp Leu Leu Ser Ser
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aag gaa gac aaa ata aaa gaa agt gaa aca ttt tca gat tca tct 1935
Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr Phe Ser Asp Ser Ser
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ccg att gag ata ata gat gaa ttt ccc acg ttt gtc agt gct aaa 1980
Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe Val Ser Ala Lys
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gat gat tct cct aaa tta gcc aag gag tac act gat cta gaa gta 2025
Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp Leu Glu Val
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tcc gac aaa agt gaa att gct aat atc caa agc ggg gca gat tca 2070
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ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc aag aat ata 2115
Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn Ile
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tat cct aaa gat gaa gta cat gtt tca gat gaa ttc tcc gaa aat 2160
Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn
      680                      685                      690

agg tcc agt gta tct aag gca tcc ata tcg cct tca aat gtc tct 2205
Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser
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gct ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa agc gct 2250
Ala Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Ala
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cac cat cac cat cac cat taa taa gctt
His His His His His His End
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2281

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<212> PRT

<213> artificial sequence

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<221> SIGNAL

$$\langle 222 \rangle \quad (-21) \dots (-1)$$

<220>

<221> CHAIN

$\langle 222 \rangle \quad (1) \dots (777)$

<223> fusion protein of truncated rat Nogo-A fragment and Strep-tag II

<220>

<221>

<222> (1) ... (767)

<223> mature truncated Nogo-A

<220>

<221>

<222> (767) ... (777)

<223> Strep-tag II affinity tag

<400> 16

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Ala	Leu	Pro 5	Ala	Ala	Ser	Glu	Pro 10	Val	Ile	Pro	Ser	Ser 15	Ala	Glu	
Leu	Phe	Lys 20	Ile	Met	Asp	Leu	Met 25	Glu	Gln	Pro	Gly	Asn 30	Thr	Val	
Ser	Ser	Gly 35	Gln	Glu	Asp	Phe	Pro 40	Ser	Val	Leu	Leu	Glu 45	Thr	Ala	
Ala	Ser	Leu 50	Pro	Ser	Leu	Ser	Pro 55	Leu	Ser	Thr	Val	Ser 60	Phe	Lys	
Glu	His	Gly 65	Tyr	Leu	Gly	Asn	Leu 70	Ser	Ala	Val	Ser	Ser 75	Ser	Glu	
Gly	Thr	Ile 80	Glu	Glu	Thr	Leu	Asn 85	Glu	Ala	Ser	Lys	Glu 90	Leu	Pro	
Glu	Arg	Ala 95	Thr	Asn	Pro	Phe	Val 100	Asn	Arg	Asp	Leu	Ala 105	Glu	Phe	
Ser	Glu	Leu 110	Glu	Tyr	Ser	Glu	Met 115	Gly	Ser	Ser	Phe	Lys 120	Gly	Ser	
Pro	Lys	Gly 125	Glu	Ser	Ala	Ile	Leu 130	Val	Glu	Asn	Thr	Lys 135	Glu	Glu	
Val	Ile	Val 140	Arg	Ser	Lys	Asp	Lys 145	Glu	Asp	Leu	Val	Cys 150	Ser	Ala	
Ala	Leu	His 155	Ser	Pro	Gln	Glu	Ser 160	Pro	Val	Gly	Lys	Glu 165	Asp	Arg	

Val	Val	Ser	Pro	Glu	Lys	Thr	Met	Asp	Ile	Phe	Asn	Glu	Met	Gln
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Met	Ser	Val	Val	Ala	Pro	Val	Arg	Glu	Glu	Tyr	Ala	Asp	Phe	Lys
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Pro	Phe	Glu	Gln	Ala	Trp	Glu	Val	Lys	Asp	Thr	Tyr	Glu	Gly	Ser
	200						205					210		
Arg	Asp	Val	Leu	Ala	Ala	Arg	Ala	Asn	Val	Glu	Ser	Lys	Val	Asp
	215						220					225		
Arg	Lys	Cys	Leu	Glu	Asp	Ser	Leu	Glu	Gln	Lys	Ser	Leu	Gly	Lys
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Asp	Ser	Glu	Gly	Arg	Asn	Glu	Asp	Ala	Ser	Phe	Pro	Ser	Thr	Pro
	245						250					255		
Glu	Pro	Val	Lys	Asp	Ser	Ser	Arg	Ala	Tyr	Ile	Thr	Cys	Ala	Ser
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Phe	Thr	Ser	Ala	Thr	Glu	Ser	Thr	Thr	Ala	Asn	Thr	Phe	Pro	Leu
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Glu	Glu	Arg	Lys	Ala	Gln	Ile	Ile	Thr	Glu	Lys	Thr	Ser	Pro	Lys
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Thr	Ser	Asn	Pro	Phe	Leu	Val	Ala	Val	Gln	Asp	Ser	Glu	Ala	Asp
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Tyr	Val	Thr	Thr	Asp	Thr	Leu	Ser	Lys	Val	Thr	Glu	Ala	Ala	Val
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Ser	Asn	Met	Pro	Glu	Gly	Leu	Thr	Pro	Asp	Leu	Val	Gln	Glu	Ala
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Cys	Glu	Ser	Glu	Leu	Asn	Glu	Ala	Thr	Gly	Thr	Lys	Ile	Ala	Tyr
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Glu	Thr	Lys	Val	Asp	Leu	Val	Gln	Thr	Ser	Glu	Ala	Ile	Gln	Glu
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Ser	Leu	Tyr	Pro	Thr	Ala	Gln	Leu	Cys	Pro	Ser	Phe	Glu	Glu	Ala
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Pro	Leu	Asn	Ser	Leu	Leu	Pro	Ser	Ala	Gly	Ala	Ser	Val	Val	Gln
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Pro	Ser	Val	Ser	Pro	Leu	Glu	Ala	Pro	Pro	Pro	Val	Ser	Tyr	Asp
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Met	Asn	Val	Ala	Leu	Lys	Ala	Leu	Gly	Thr	Lys	Glu	Gly	Ile	Lys
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Glu	Pro	Glu	Ser	Phe	Asn	Ala	Ala	Val	Gln	Glu	Thr	Glu	Ala	Pro
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Tyr	Ile	Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser
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Thr	Glu	Pro	Ser	Pro	Asp	Phe	Ser	Asn	Tyr	Ser	Glu	Ile	Ala	Lys
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Glu	Ser	Phe	Gln	Pro	Asn	Leu	His	Ser	Thr	Lys	Asp	Ala	Ala	Ser
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Glu	Val	Ser	Asp	Lys	Ser	Glu	Ile	Ala	Asn	Ile	Gln	Ser	Gly	Ala
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	755						760					765		
Ser	Ala	Trp	Arg	His	Pro	Gln	Phe	Gly	Gly					
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Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val
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 Asp Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly
 170 175 180
 Lys Asp Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr
 185 190 195
 Pro Glu Pro Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala
 200 205 210
 Ser Phe Thr Ser Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro
 215 220 225
 Leu Leu Glu Asp His Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys
 230 235 240
 Ile Glu Glu Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr Ser Pro
 245 250 255
 Lys Thr Ser Asn Pro Phe Leu Val Ala Val Gln Asp Ser Glu Ala
 260 265 270
 Asp Tyr Val Thr Thr Asp Thr Leu Ser Lys Val Thr Glu Ala Ala
 275 280 285
 Val Ser Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu
 290 295 300
 Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr Gly Thr Lys Ile Ala
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 Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser Glu Ala Ile Gln
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 Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser Phe Glu Glu
 335 340 345
 Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu
 350 355 360
 Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val Val
 365 370 375
 Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
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 Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu
 395 400 405
 Ala Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile
 410 415 420
 Lys Glu Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala
 425 430 435
 Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu
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 Ser Thr Glu Pro Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala
 455 460 465

Lys Phe Glu Lys Ser Val Pro Glu His Ala Glu Leu Val Glu Asp
 470 475 480
 Ser Ser Pro Glu Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser
 485 490 495
 Ile Pro Glu Val Pro Gln Thr Gln Glu Glu Ala Val Met Leu Met
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 Lys Glu Ser Leu Thr Glu Val Ser Glu Thr Val Ala Gln His Lys
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 Glu Glu Arg Leu Ser Ala Ser Pro Gln Glu Leu Gly Lys Pro Tyr
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 Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn Asp Asp Leu
 575 580 585
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 590 595 600
 Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe Val
 605 610 615
 Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp
 620 625 630
 Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly
 635 640 645
 Ala Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe
 650 655 660
 Lys Asn Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe
 665 670 675
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 Asn Val Ser Ala Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val
 695 700 705
 Lys Ser Ala Trp Arg His Pro Gln Phe Gly Gly
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